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11/06

#10

OIPE

RAW SEQUENCE LISTING   DATE: 08/14/2001
PATENT APPLICATION: US/09/759,281B   TIME: 09:15:52

Input Set : A:\41826cip.app
Output Set: N:\CRF3\08142001\I759281B.raw

ENTERED

```
 3 <110> APPLICANT: PEREGRINO FERREIRA, PAULO CESAR
 4        KROON, ERNA GEESSIEN
 5        PIMENTA DOS REIS, JENNER KARLISSON
 6        FORTES FERRAZ, ISABELLA BIAS
 7        CERQUEIRA LEITE, ROMULO
 9 <120> TITLE OF INVENTION: METHOD AND COMPOSITION FOR THE DIAGNOSIS OF EQUINE
10        INFECTIOUS ANEMIA VIRUS DISEASE BY USING THE
11        RECOMBINANT CAPSID PROTEIN VIRUS (P26)
13 <130> FILE REFERENCE: 41826 CIP
15 <140> CURRENT APPLICATION NUMBER: 09/759,281B
16 <141> CURRENT FILING DATE: 2001-01-16
18 <150> PRIOR APPLICATION NUMBER: 09/331,262
19 <151> PRIOR FILING DATE: 1999-07-13
21 <150> PRIOR APPLICATION NUMBER: PCT/BR97/00081
22 <151> PRIOR FILING DATE: 1997-12-19
24 <150> PRIOR APPLICATION NUMBER: PI 9606273-8
25 <151> PRIOR FILING DATE: 1996-12-18
27 <160> NUMBER OF SEQ ID NOS: 1
29 <170> SOFTWARE: PatentIn Ver. 2.1
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 318
33 <212> TYPE: PRT
34 <213> ORGANISM: Equine infectious anemia virus
36 <400> SEQUENCE: 1
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41              20                  25                  30
43 Leu Thr Thr Gly Asn Cys Asn Trp Ala Leu Ser Leu Val Asp Leu Phe
44          35                  40                  45
46 His Asp Thr Asn Phe Val Lys Glu Lys Asp Trp Gln Leu Arg Asp Val
47      50                  55                  60
49 Ile Pro Leu Leu Glu Asp Val Thr Gln Thr Val Ser Gly Gln Glu Arg
50  65                  70                  75                  80
52 Glu Ala Phe Glu Arg Thr Trp Trp Ala Ile Ser Ala Val Lys Met Gly
53              85                  90                  95
55 Leu Gln Ile Asn Asn Val Val Asp Gly Lys Ala Ser Phe Gln Leu Leu
56              100                 105                 110
58 Arg Ala Lys Tyr Glu Lys Lys Thr Ala Asn Lys Lys Gln Ser Glu Pro
59              115                 120                 125
61 Ser Glu Glu Tyr Pro Ile Met Ile Asp Gly Ala Gly Asn Arg Asn Phe
62      130                 135                 140
64 Arg Pro Leu Thr Pro Arg Gly Tyr Thr Thr Trp Val Asn Thr Ile Gln
65 145                 150                 155                 160
67 Thr Asn Gly Leu Leu Asn Glu Ala Ser Gln Asn Leu Phe Gly Ile Leu
68              165                 170                 175
70 Ser Val Asp Cys Thr Ser Glu Glu Met Asn Ala Phe Leu Asp Val Val
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71              180             185             190
73 Pro Gly Gln Ala Gly Gln Lys Gln Ile Leu Leu Asp Ala Ile Asp Lys
74         195             200             205
76 Ile Ala Asp Asp Trp Asp Asn Arg His Pro Leu Pro Asn Ala Pro Leu
77     210             215             220
79 Val Ala Pro Pro Gln Gly Pro Ile Pro Met Thr Ala Arg Phe Ile Arg
80 225             230             235             240
82 Gly Leu Gly Val Pro Arg Glu Arg Gln Met Glu Pro Asn Cys Val Val
83             245             250             255
85 Gln Ser Phe Gly Val Ile Gly Gln Ala His Leu Glu Leu Pro Arg Pro
86             260             265             270
88 Asn Lys Arg Ile Arg Asn Gln Ser Phe Asn Gln Tyr Asn Cys Ser Ile
89         275             280             285
91 Asn Asn Lys Thr Glu Leu Glu Thr Trp Lys Leu Val Lys Thr Ser Gly
92     290             295             300
94 Val Thr Pro Leu Pro Ile Ser Ser Glu Ala Asn Thr Gly Leu
95 305             310             315
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/759,281B**

DATE: 08/14/2001
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Input Set : **A:\41826cip.app**
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BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]
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Score =  444 bits (1143), Expect = e-123
Identities = 212/243 (87%), Positives = 229/243 (93%)
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Sbjct:10   GNPLTWSKALKKLQKVTVQGSQKLTTGNCNWALSLVDLFHDTNFVKQKDWQLRDVIPLLQ 69

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           DVTQT+SGQ+R+AF+RTWWAISAVKMGLQINNVVDGKASFQLLRAKY+KKTANKKQS+PS
Sbjct: 70  DVTQTVSGQQRQAFQRTWWAISAVKMGLQINNVVDGKASFQLLRAKYQKKTANKKQSQPS 129

Query: 122 EEYPIMIDGAGNRNFRPLTPRGYTTWVNTIQTNGLLNEASQNLFGILSVDCTSEEMNAFL 181
           ++YPIMIDGAGNRNFRPLTPRGYTTWVNTIQTNGLLN+ASQNLFGILSVDCTS++MNAFL
Sbjct: 130 QQYPIMIDGAGNRNFRPLTPRGYTTWVNTIQTNGLLNQASQNLFGILSVDCTSQQMNAFL 189

Query: 182 DVVPGQAGQKQXXXXXXXXXXXXXXXXXNRHPLPNAPLVAPPQGPIPMTARFIRGLGVPRERQ 241
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Sbjct: 190 DVVPGQAGQKQILLDAIDKIADDWDNRHPLPNAPLVAPPQGPIPMTARFIRGLGVPRQRQ 249

Query: 242 MEP 244
           M+P
Sbjct: 250 MQP 252
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Query: ACCESSION   M16575 K03334 M11337 M14855
REFERENCE   7   (bases 1 to 8344)
Kawakami,T., Sherman,L., Dahlberg,J., Gazit,A., Yaniv,A., Tronick,S.R.
and Aaronson,S.A. Nucleotide sequence analysis of equine infectious
anemia virus proviral DNA. Virology 158 (2), 300-312 (1987)

Sbjct: proposed sequence of instant invention

ANNEX 2

```
LOCUS       EIAVCG              8407 bp ss-RNA      linear    VRL 11-AUG-1995
DEFINITION Equine infectious anemia virus proviral DNA, complete
genome.
ACCESSION  M16575 K03334 M11337 M14855
VERSION    M16575.1  GI:323836
KEYWORDS    complete genome; env protein; gag protein; glycoprotein; pol
            protein; polymerase.
SOURCE      Equine infectious anemia virus
 ORGANISM  Equine infectious anemia virus  Viruses; Retroid viruses;
Retroviridae; Lentivirus; Equine  lentiviruses.
REFERENCE 6  (bases 1 to 8407)
AUTHORS    Kawakami,T., Sherman,L., Dahlberg,J.E., Gazit,A., Yaniv,Y.,
           Tronick,S.R. and Aaronson,S.A.JOURNAL   Unpublished (1987)
REFERENCE   7  (bases 1 to 8344)
AUTHORS    Kawakami,T., Sherman,L., Dahlberg,J., Gazit,A., Yaniv,A.,
           Tronick,S.R. and Aaronson,S.A. Nucleotide sequence analysis
           of equine infectious anemia virus proviral DNA. Virology 158
           (2), 300-312 (1987)
MEDLINE    87236196    PUBMED    3035786
COMMENT    Original source text: Equine infectious anemia virus (EIAV)
proviral DNA, (clones 1369 and 409-2 [1]). [2]  sites; peptide coding
regions. [6]  revises [1]. [8]  sites; sequence correction position
5348. Draft entry and computer-readable sequence for [6] kindly
provided by S.Tronick, 10-NOV-1987.


FEATURES                Location/Qualifiers
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    variation           342
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                        /replace="t"
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                        /note="465 is the position of the first start
codon in the open reading frame/codon_start=1/product="gag
protein/protein_id="AAB59861.1/db_xref="GI:323837/translation="

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LLRAKYEKKTANKKQSEPSEEYPIMIDGAGNRNFRPLTPRGYTTWVNTIQTNGLLNEA
SQNLFGILSVDCTSEEMNAFLDVVPGQAGQKQILLDAIDKIADDWDNRHPLPNAPLVA
PPQGPIPMTARFIRGLGVPRERQMEPAFDQFRQTYRQWIIEAMSEGIKVMIGKPKAQN
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C.